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Minimum
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Q9w4b8 drosophila

Q9sew4 juglans reg

Q9vr08 drosophila

Q9m8t1 arabidopsis

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ALIGNMENTS

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Best Local Similarity
022120
022120;
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Morassutti C., Warchetti S., De Amicis F., Zaina G., Zanetti M.;

"Expression and purification of the antimicrobial peptide SMAP-29
tobacco transgenic plants by SceWMA-intein system.";

Submitted (MAR-2000) to the EMBL/GenBank/DDEJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean).

Glycine max (Soybean).

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eddicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Glycine.

MCBI_TaxID=3847;
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ALPHA, ALPHA'-TYPE BETA-CONGLYCININ (FRAGMENT).
BCSP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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96.9%;
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Pred. No. 3.2e-14;
                                             PRT;
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                                                                                                                                                                                               Rogers W.O., Gowda K., Sacci J., Hoffman S.L.; "Construction and immunogenicity of DNA vaccine plasmids Plasmodium vivax candidate vaccine antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ALPHA SUBUNIT OF BETA CONGLYCININ.
                                                                                              VARIANT
                                                                                                                                       PRINTS;
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01-MAY-1999
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Submitted (NOV-1997) to the
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                                                                                                                                                                 INTERPRO; IPRO00884; INTERPRO; IPRO02035;
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Mismatches
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                                                                                                                                                                                          databases
                                           CRC64;
               Length 556;
                                                                                                                                                                                                                                                            Plasmodium
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Indels
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Gaps
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2;
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RESULT
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Best Local (
                                                                                                                                                                                       Eukaryota; Metazoa; A; Pterygota; Neoptera; Pterygota; Neoptera; Ephydroidea; Drosophi
                                                                                                                                                                                                                                                                                                                           Q9W4BB
Q9W4BB;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
CG3239 PROTE
CG3239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
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SEQUENCE
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  MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Amanatides P.G., Scherer S.E., Li P.W George R.A., Lewis S.E., Richards S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax candidate vaccine antigens.";
Vaccine 17:3136-3144(1999).
EMBL; AF063137; AAC97485.1; -.
INTERPRO: IPR000884: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99389346; PubMed=10462250; Rogers W.O., Gowda K., Hoffman S.L "Construction and immunogenicity o
                                                                                                             SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CLQSCNSERDSYRNQACHARCNLLKVEKEECEEGE-----IPRPRPRPQHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
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                                                                                                                                                                                                                                                                                                                                                         PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00453;
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                                                                                                                                                                                                                                           Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vivax.
Alveolata;
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(TrEMBLrel.
(TrEMBLrel.
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ilidae; Drosophila.
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Pred. No. 1.2;
4; Mismatches
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., Evans C.A., Gocayne J.
.W., Hoskins R.A., Galle
., Ashburner M., Hendersc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemosporida;
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                                                                                                                                                                                                                                                                                                                                                                               update)
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  No., Galle R.F., Henderson S.N.
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RA Beeson K. Y., Benos P. V., Berman B. P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Davies P., Carg N.S., Gelbart W.M., Glasser K.,

RA Dodson K., Daviel S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T. J., Hernandez J.R., Houck J.,

RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Ramington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Shen R., Sheng L., Sheng L., Sheng L.,

RA Sheng S., Jano Q., Zhong S., Zhou X., Smith H.O.,

RA Sheng S., Sheng R., Sheng S., Sheng L.,

Ra Sheng S., Sheng R., Sheng S., Sheng Q., Zhong Q.,
                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                  OSSEWA;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                   Juglans regia (English walnut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                     Q9SEW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
SEQUENCE 719 AA; 83325 MW; 6C3DE7B4380
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  SEQUENCE
                                       NCBI_TaxID=51240;
                                                                               Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                        ECEE---GEIP-----RPRPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                              Juglandaceae;
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                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LQSCNSERDS------YRNQACHA--RCNLLKVEKE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.4%; 27.1%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Baldwin D.,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 20196006; PubMed = 10731132;

A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A Ceorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

A Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

A Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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                                                                                                                   Shue B.C.,
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Pterygota;
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allergen.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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P02853; 2PHL.
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                           , Siden-Kiamos I., Simpson M., Skupski M.P.,
Spradling A.C., Stapleton M., Strong R., Sun
R., Tector C., Turner R., Venter E., Wang A.
., Wassarman D.A., Weinstock G.M., Weissenba
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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ilidae; Drosophila
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Venter E., Wang ....
Venter E., Wang ....
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Matches 17
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Best Local Similarity
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INTERPRO: IPRO00561; -.
INTERPRO: IPRO00561; -.
INTERPRO: IPRO0088; EGF: 28.
PFAM: PF00008; EGF: 28.
PROSITE: PS00010; ASX HTDROXYL: 1
PROSITE: PS00022; EGF-1; 1.
PROSITE: PS01186; EGF-2; 18.
PROSITE: PS01187; EGF-CA: 17.
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Q9M8T1;
01-OCT-2000 (TrEMBLrel 1
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F13E7 16.
                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AC018363; AAF26970.1; -. SEQUENCE 963 AA; 105391 MW; D2041DC304280:
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., B.
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F13E7 genor
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sy
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE003576; AAF51000.1; -.
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Ye J., Yeh R.-F.,
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| PQ 2879
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                                                           EEGEI 43
                                                                                  ENPSNKKSLTDRTLSRMQSCMKEEDAKEGKACSG---
                                                                                                           ENPKHNKCL-----QSCNSERDSYRNQACHARCNLLKVEKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yeh R.F., Zaveri J.S., Zhan M., Zhang S., Zhao X.H., Zhong F.N., Zhong W., Zhou X., Zhug R., Zhug R., Zhug R., Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P35555;
                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conser
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                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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388637 MW;
                                                                                                                                              21.0%;
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15,
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Last sequence update)
Last annotation updat
                                                                                                                                  Score 66; DB Pred. No. 5.3; Mismatches
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Pred.
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                                                                                                                                                           DB 10;
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                                                                                  -TEKENAFSVSYGEGEVDVET
                                                                                                                                    13;
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I databases.
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                                                                                                                                                           Length 963;
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                                                                                                                                                                                                                                                                                                                                                  Spermatophyta;
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Smith
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Best Local
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042918;
01-JAN-1999
01-JAN-1999
01-OCT-2000
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Q94727;
Q1-FEB-1997
                                                                                                                                                                                                                                                                                                      01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE ALPHA-AMYLASE C16A3.13 PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
NON_TER
SEQUENCE
             SIGNAL
                       PFAM; PF00128; alpha-amylase; 1.
Hypothetical protein; Hydrolase;
Calcium; Glycoprotein; Signal.
                                                                        EMBL; AL021748; CAA16864.1; HSSP; P10529; 7TAA.
                                                                                                                                    Wood V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt R.; Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
-i- CATALYTIC ACTIVITY: ENDOHYDROLVSIS OF 1, 4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-i- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY (BY
                                                                                           SIMILARITY).

-I- SIMILARITY: TO THE FAMILY 13

THE ALPHA ANYLASE FAMILY.
                                                                                                                                                                                          STRAIN=972;
Wood V., Ra
                                                                                                                                                                                                                                                                                           SPBC16A3.13
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Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. THROMBOSPONDIN-RELATED
                                                                                                                                                                                                                                                                Eukaryota; Fungi;
                                                                                                                                                                                                                                                                              Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00090; tsp_1; 1. PFAM; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biochem. Parasitol. 84:13-24(1997). EMBL; U64901; AAC47463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anonymous protein (TRAP) gene from Plasmodium
vivax and Plasmodium gallinaceum.";
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01-OCT-2000
                                                              INTERPRO; IPRO00461; -.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Templeton T.J., Kaslow D.C.;
"Cloning and cross-species comparison of the thrombospondin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97193932; PubMed=9041517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5855;
                                                                                                                                                                                                                                         NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000884; -. IPR002035; -.
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510 AA;
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                    Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510
                                                                                                                                                                                                                                                                pombe (Fission yeast).
scomycota; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55601 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%;
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. 15, Last annotation update)
anonymous protein (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02,
02,
                                                                                                                                                                                                                                                      Schizosaccharomyces
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; Pred. No. 3.5;
3; Mismatches
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             POTENTIAL.
PUTATIVE ALPHA-AMYLASE
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                                     Glycosidase;
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                                    Carbohydrate metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 510;
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Best Local
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Best Local
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         Q90865;
Q90865;
01-NOV-1996
01-NOV-1996
01-OCT-2000
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01-JUL-1997
01-OCT-2000
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STRAIN=C57BL6;
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                                                                                                                                                                                                                                   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             Aoki N.;
                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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nes 16; Conserv
                                                             12
                                                                                                13 NSERDSYRNQACHARCNLLKVEKEECEEGEI-PRP--RPRPQHP
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                                                                                                                                                                                                                                                                                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                             HKCKEHCSCHHDKFPRPVPH----NGTKPDHKPWKHEEHCHHGKFPRPVPHNGTKPDH
                                                                                    NSFTEKYETEG--QRINLKKVAREQRKAKELPPKPSSRPQPAHP
                                                                                                                       . Similarity
17; Conser
6 (TrEMBLrel. 01, Created)
6 (TrEMBLrel. 01, Last sequence update)
0 (TREMBLrel. 15, Last annotation update)
GROWTH FACTOR-LIKE/MACROPHAGE STIMULATING PROTEIN.
                                                                                                                                                                                                                                                                                                Metazoa;
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                                                                                                                       20.5%;
ilarity 38.6%;
Conservative
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553
229
229
495
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1143
1187
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                                            PRELIMINARY;
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                                                                                                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                       TISSUE-SKIN;
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3 553
60 314
724
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409
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Rodentia;
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28.1%;
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04,
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                                                                                                                      Score 64.5; DI
Pred. No. 3.2;
8; Mismatches
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Pred. No. 5;
8; Mismatches
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                                            PRT;
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                                                                                                                              No. 3
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Best Local :
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                                                                                                                                                                                                                                     Q20155
Q20155;
Q1-NOV-1996
Q1-MAY-1999
Q1-JUN-2000
                   Hypothetical protein; Alternative splicing.

VARSPLIC 1 38 MISSING (IN ISOFORM B).

VARSPLIC 39 52 AFSSNYIDQPGLLF -> MSIENYHLSFL
                                                              EMBL; Z74033; CAA98475.1;
EMBL; Z74033; CAA98476.1;
INTERPRO; IPRO00571;
                                                                                                      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN
                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00024; PAN; 1.
PFAM; PF000051; kringle; 4.
PFAM; PF000089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR007722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGF1/MSP.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Thomporta: Metazoa; Chordata; Craniata; Vert
SEQUENCE
                                                                                                                                                                                                                   F38B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       during early chick development.";
Dev. Genet. 17:90-101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria;
Gallus.
                                                      PFAM; PF00642; zf-CCCH;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=6239;
[1]
                                                                                                                                                                                                                              F38B7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00021; KRINGLE_1; UNKNOWN_4
PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00747; 1CEA.
MEROPS; S01.977; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X84043; CAA58862.1; HSSP; P00747; 1CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thery C., Sharpe M.J., Batley S.J., Saxpression of HGF/SF, HGF1/MSP, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96029010; PubMed=7554499; Thery C., Sharpe M.J., Batley S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                         Lennard
                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                          53 PER 55
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                                                                                                                                                                                                                                                                                                                                                                                                  2 NPKHNKC------LQSCNSERDSYRNQACHARCNLLKVEKEECEEGEIPRPRPRPRPQH
                                                                                             OF FORM A.
                                                                                                                                                                                                                                                                                                                                      PDK
                                                                                                                                                                                                                                                                                                                                                                             NVRHQSCGIKKCEDAVCMTCNGE--DYRGFVDHTESG----TECQRWDLQHPHKHPYH
                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
15; Conserv
                                                                                                                                                                                                                             PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IPR000001; -.; IPR001254; -.; IPR001314; -.; IPR003014; -.
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 414
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                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                           Nematoda;
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Caenorhabditis.
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Pred.
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D8B29D29A9E39583 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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No. 6.1;
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mes; Phasianidae; Phasiani
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Best Local Similarity 35.9
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01-AUG-1998 (TrEMBLrel. (
01-AUG-1998 (TrEMBLrel. (
01-MAY-2000 (TrEMBLrel. 1
Y43F4A.1 PROTEIN.
                                                                                                                                                                                                                                                                                    Q9KK20;
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INTERPRO; IPRO01577; -.
INTERPRO; IPRO01577; -.
PFAM; PF01457; Peptidase_M8; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                    01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
SURFACE PROTEIN PSPC.
       Streptococcus
                                                                       Streptococcus pneumoniae.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhamer E., Staden R., Sulston J.,
Thioremaker E., Staden R.,
Thioremaker E., Staden
                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   062446
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EMBL; 299271; CAB16471.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firmicutes;
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                                   Bacillus/Clostridium group; Streptococcaceae;
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Last annotation update)
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Pred. No. 5.1;
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Best Local
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"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154036; AAF73808.1; -.
SEQUENCE 519 AA; 58731 MW; 7E187:95825AFD1E CRC64;
                                                                                                                                                                                                                                                      STRAIN=G99;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=1313;
[1]
                                                    211
269 APAPQ-PEK 276
                          47
                                                                             3 PKHNKCLQSCNSERDSYRNQACHARCNLLKVEKEECEE-----
                          RPRPQHPER 55
                                                    PRDEQKIKQAEAEVES - - KQAEATRLKKIKTDREEAEEEAKRRADAKEQGKPKPAEQPQP 268
                                                                                                        1 Similarity
19; Conserv
                                                                                                        Conservative
                                                                                                                    19.8%;
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Pred. No. 8.1;
11; Mismatches
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Search completed: March 1, 2001, 16:17:18 Job time: 456 sec